

Figure 1

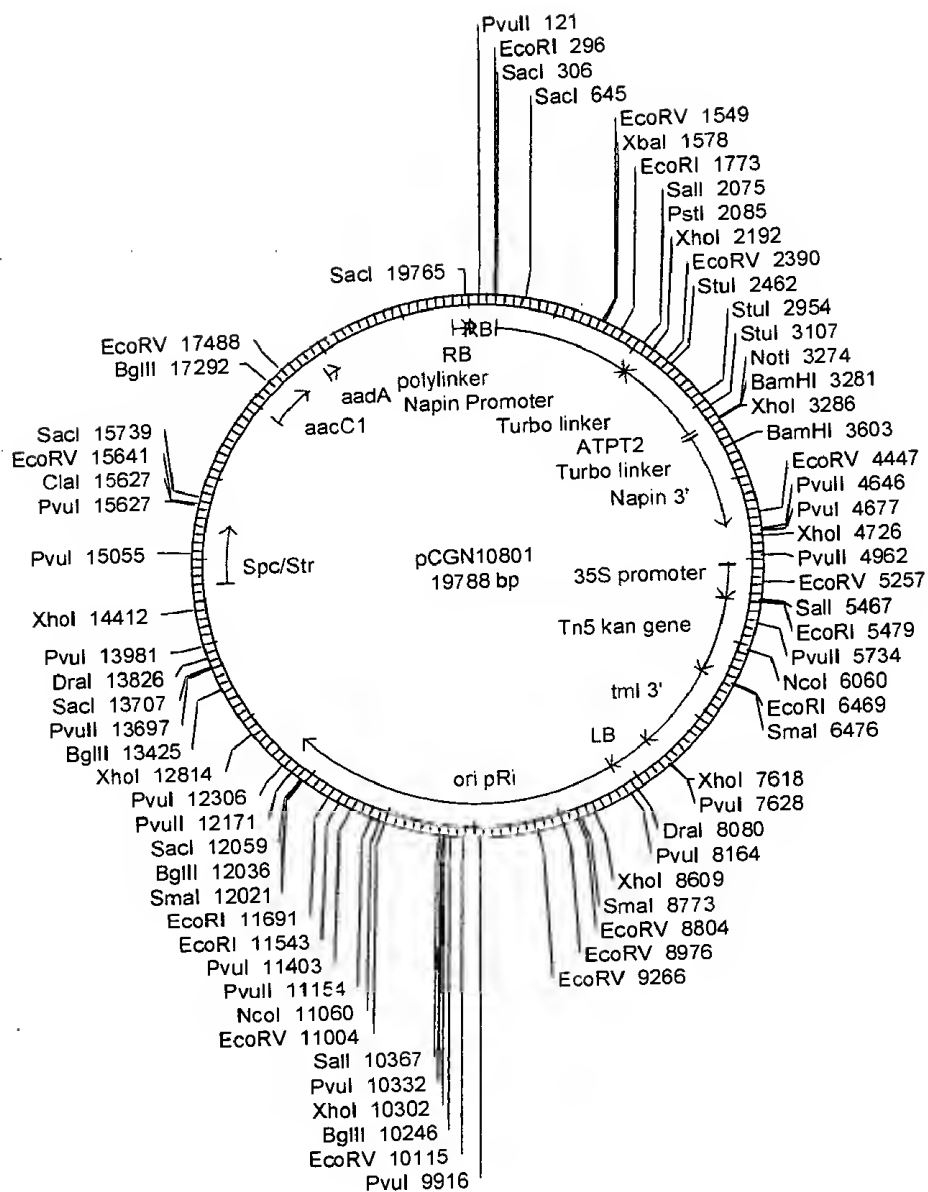


Figure 3

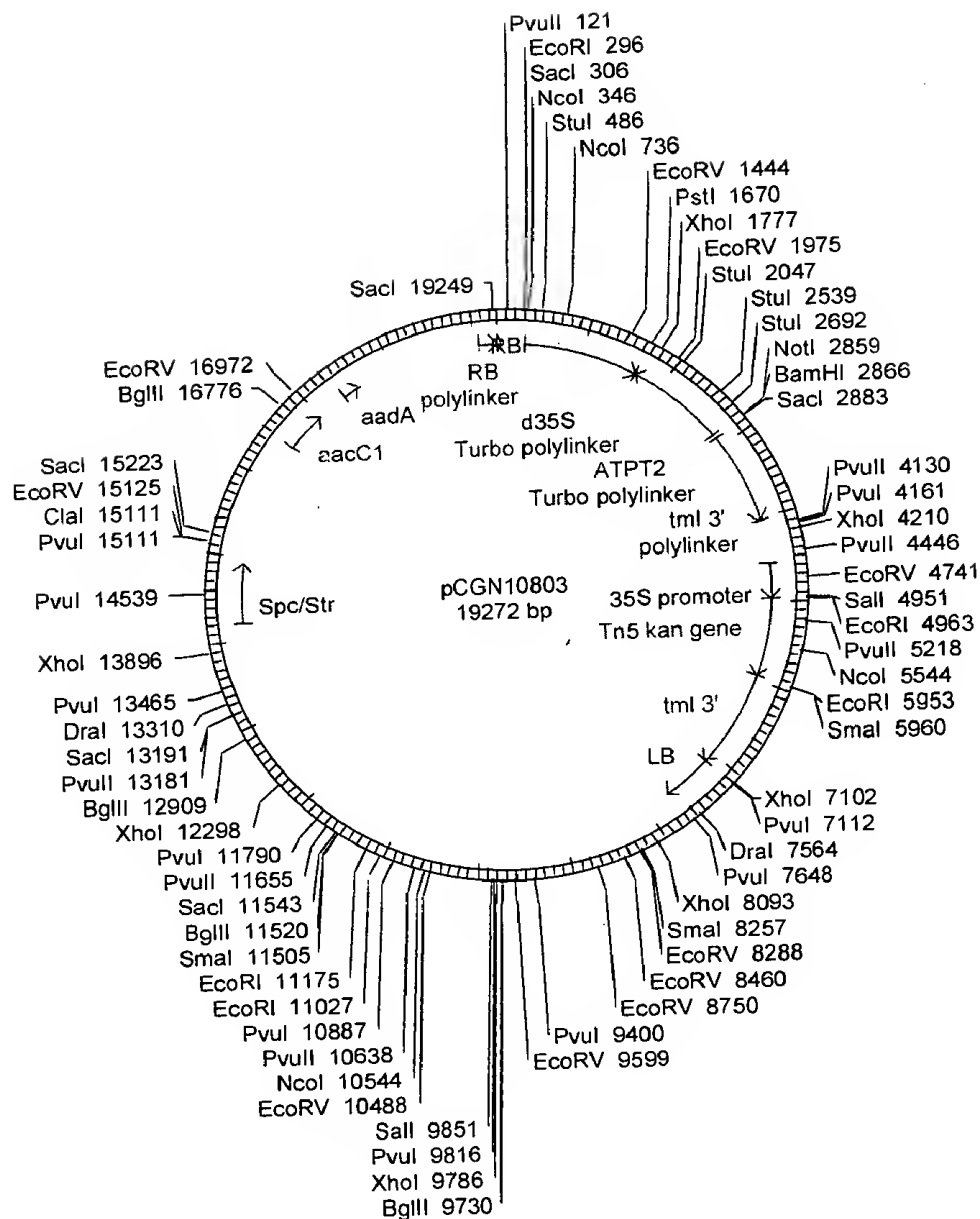


Figure 4

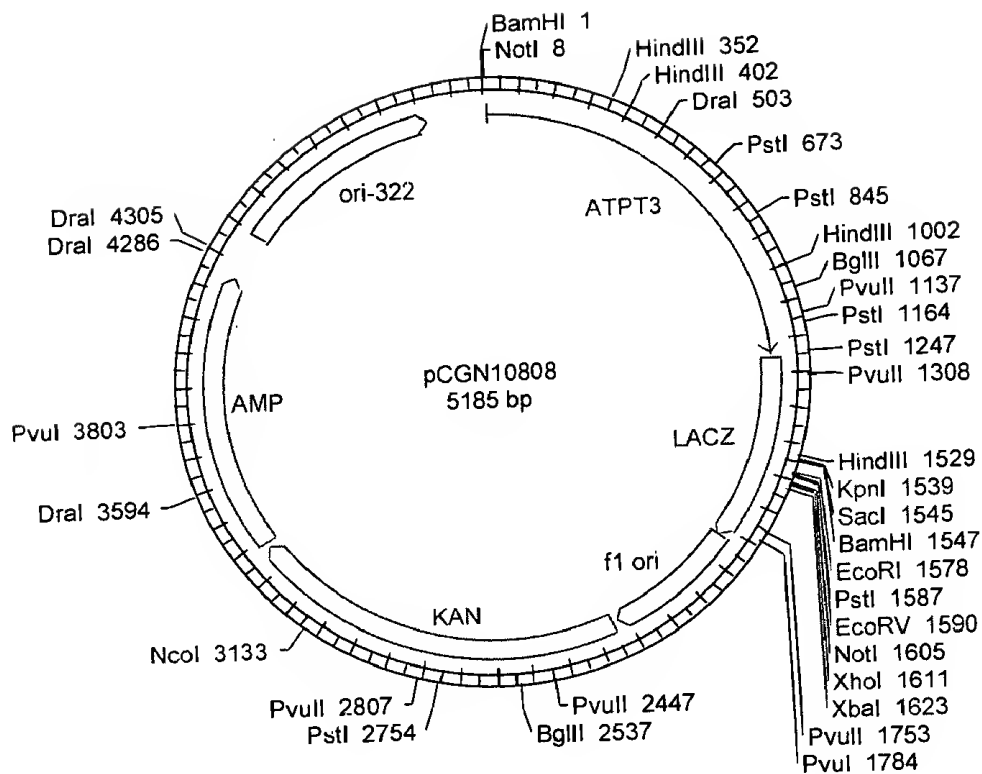


Figure 7

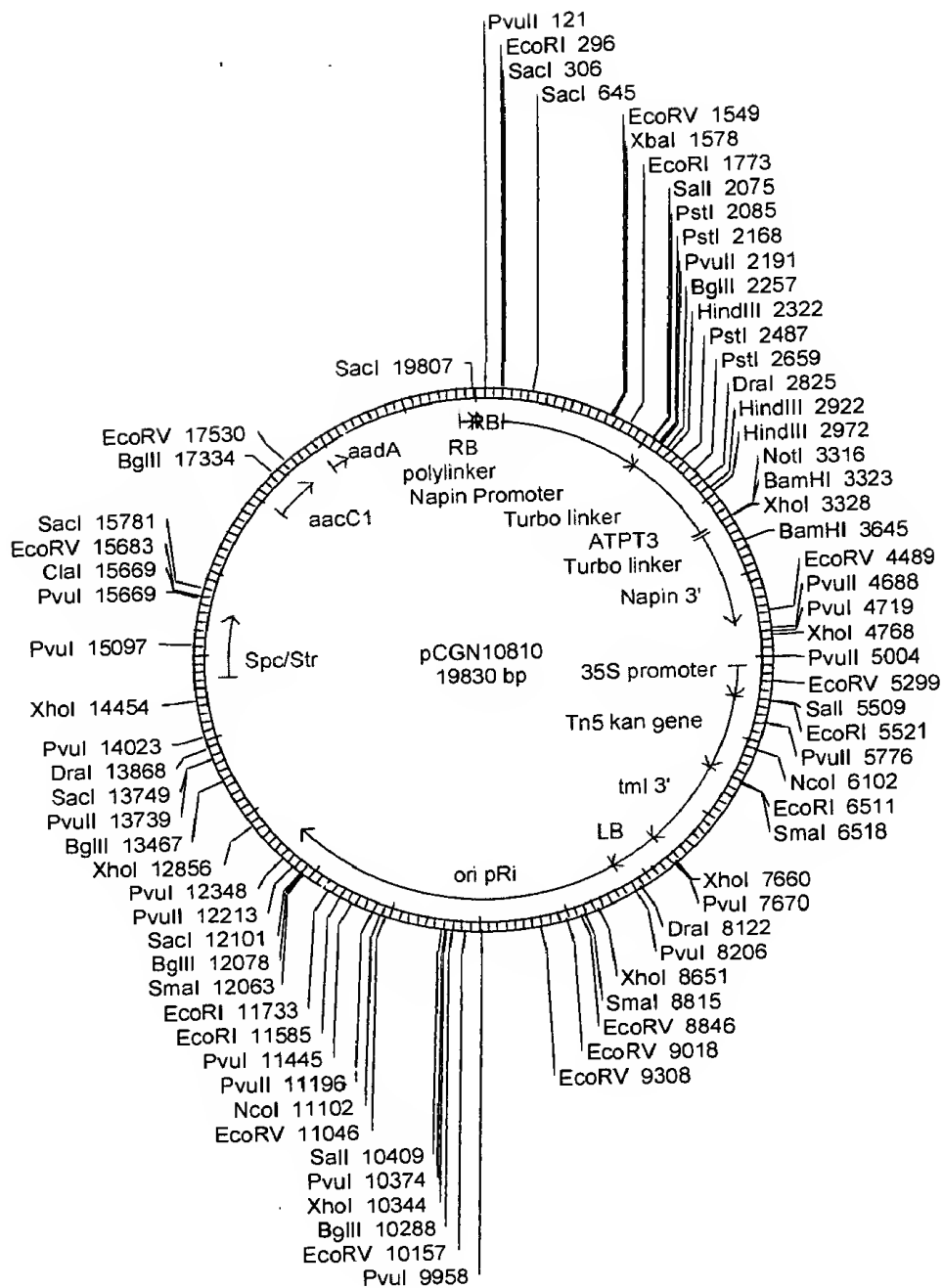


Figure 9

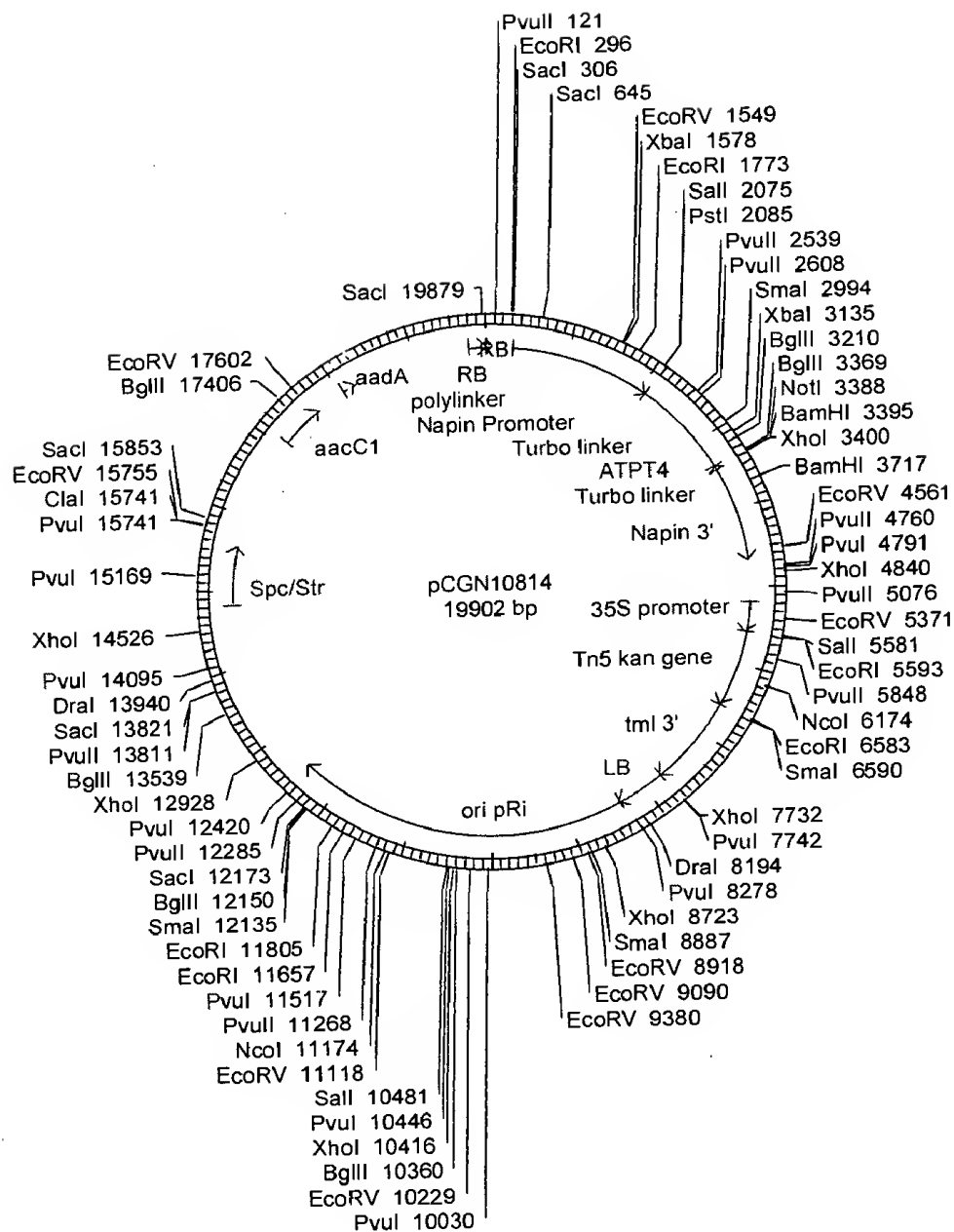


Figure 13

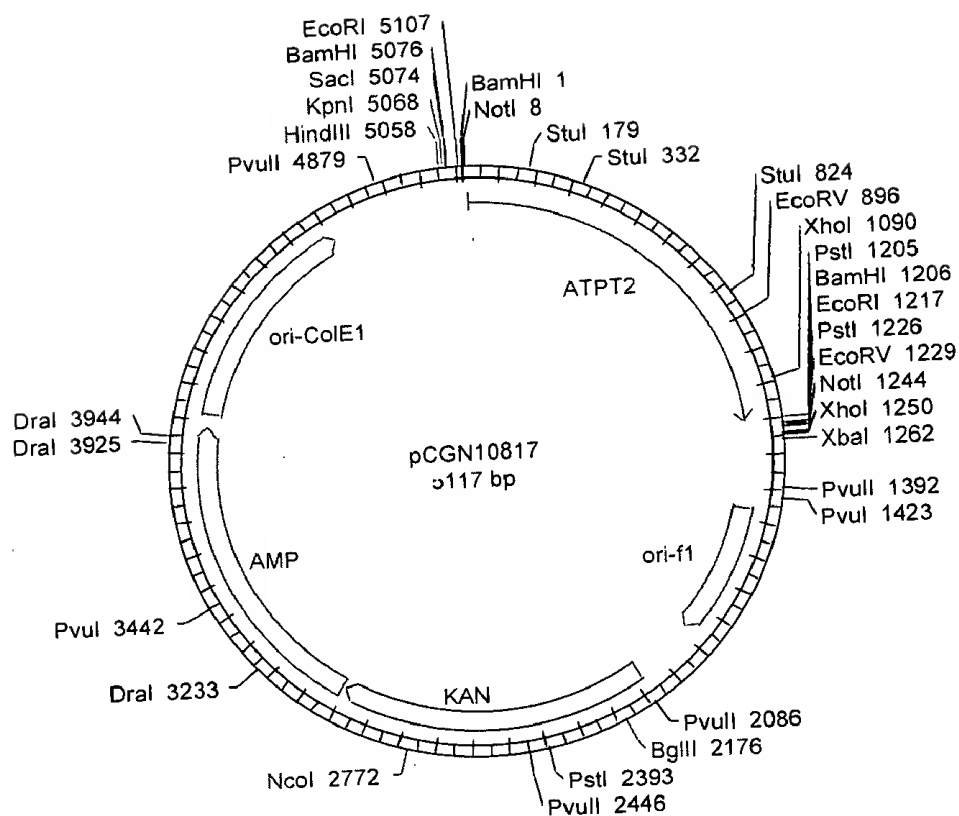


Figure 16

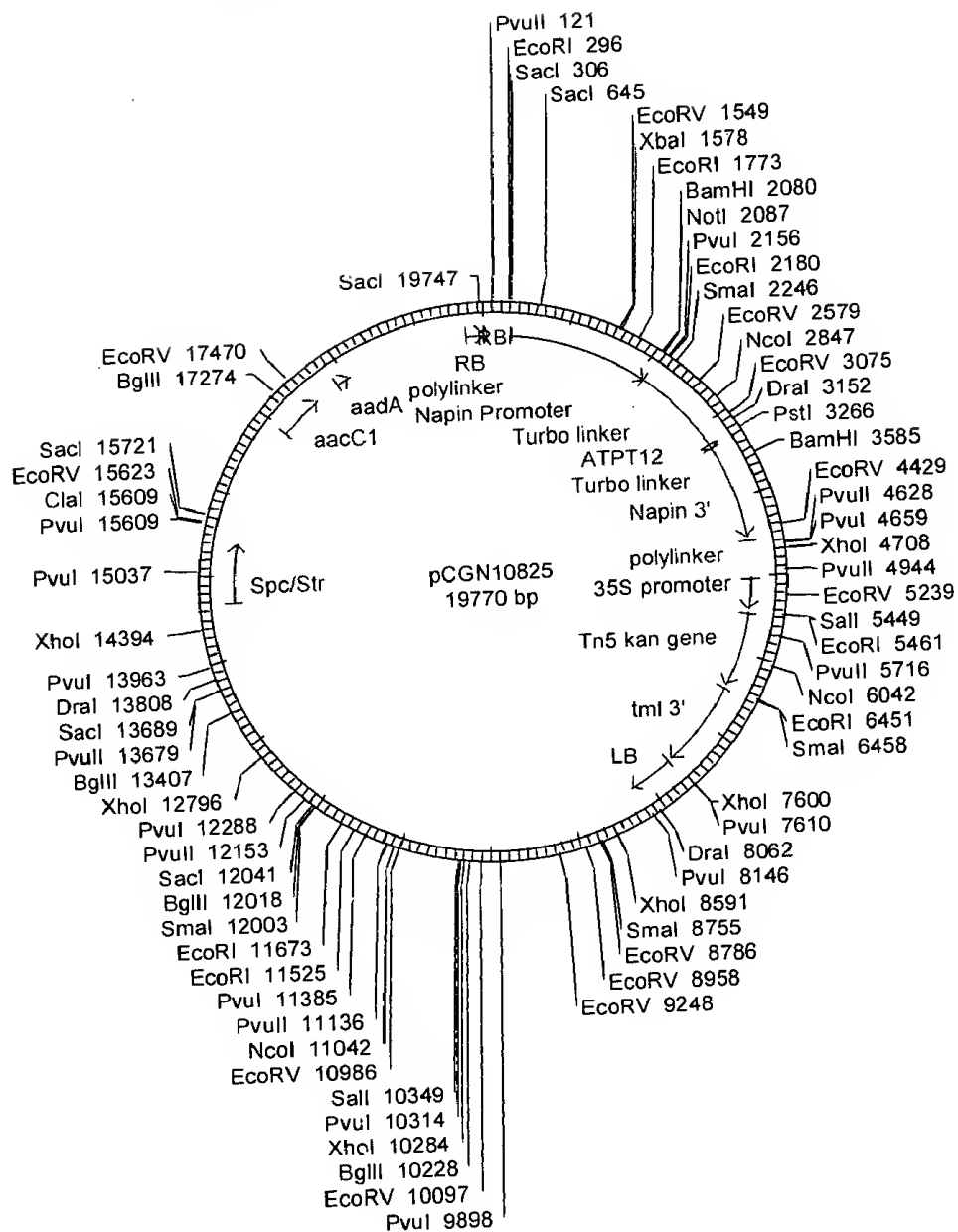


Figure 19

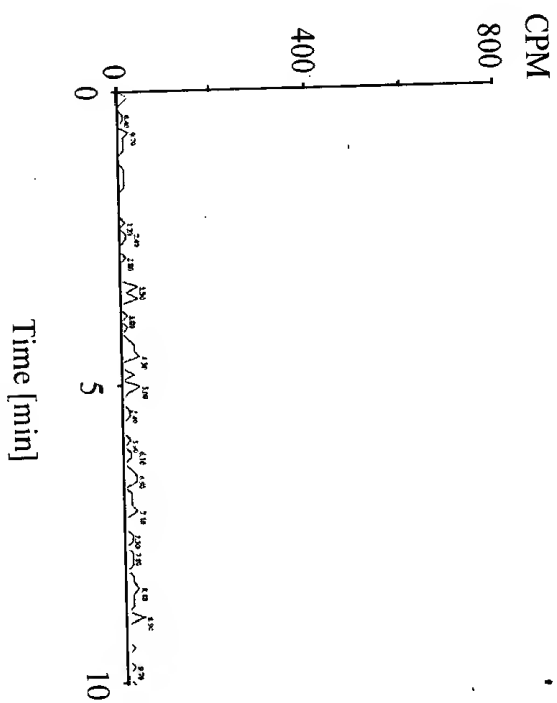
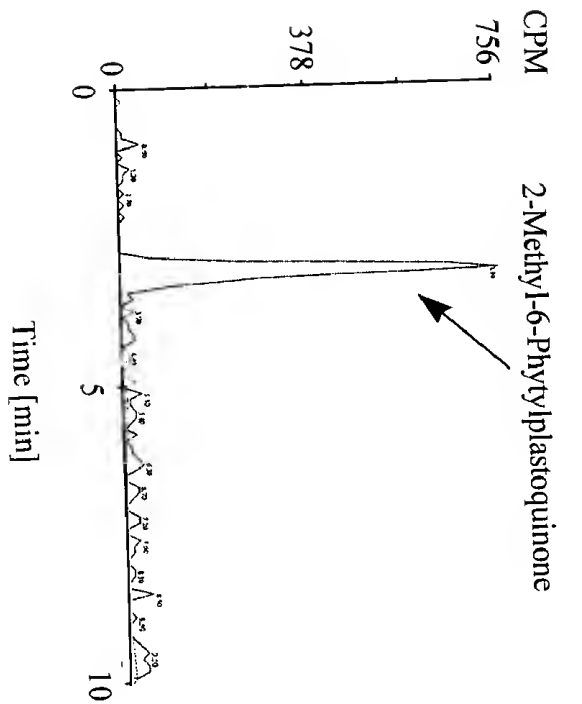
ATP12 : ----- * 20 * 40 * 60 * 80
 SLR1736 : -----MESLSSSLVSAAGFCWKQKONLKLHSLSEIRVLRCDSKVVAKPKFRNNLVPRPDGSSLLYPKHKSREVRNATAGQ : 80
 ATP3 : -----MAFFGLSRVSRLLKSSVVTPESSSALLQSHKSLNPVTTHYNPTKCYPSWNNQVWSKREIHOKEFEVGNRYRLICGMSS : 89
 SLR0926 : -----MRRSVYRFSRISVSSSLPNRLIPMSREICAVNSFSQP-----PVSTSTAKLGITGVRSNDANRVATA : 67
 ATP4 : -----MRRSVYRFSRISVSSSLPNRLIPMSREICAVNSFSQP-----PVSTSTAKLGITGVRSNDANRVATA : 67
 SLR1899 : -----MTSILNTVSTIHSSRVTSDRVGLSLRNSDVEFT-----RRSGFSTLIESPGRFRVAAETDT : 63
 ATP12 : -----MTSILNTVSTIHSSRVTSDRVGLSLRNSDVEFT-----RRSGFSTLIESPGRFRVAAETDT : 63
 SLR0056 : -----MTSILNTVSTIHSSRVTSDRVGLSLRNSDVEFT-----RRSGFSTLIESPGRFRVAAETDT : 63
 ATP8 : -----MTSILNTVSTIHSSRVTSDRVGLSLRNSDVEFT-----RRSGFSTLIESPGRFRVAAETDT : 63
 SLR1518 : -----MTSILNTVSTIHSSRVTSDRVGLSLRNSDVEFT-----RRSGFSTLIESPGRFRVAAETDT : 63

ATP12 : ----- * 100 * 120 * 140 * 160 * 1
 SLR1736 : -----PEAFDSNSKOK-----SFRDSFPAFYR-----FSRPHTEIGTVLSILS-----VSFLAVEKVS--DISPLFTGILE : 140
 ATP3 : -----SSVLEGRPKKDDKEKSDGVVKKASWIDLYLPEEVRGYAKTARLDKPIGTWLLAWPCMS-----IALADPGS--IPSEKYMALFEGC : 170
 SLR0926 : -----MVAQTPSSP-----PLWITIIYL-----LRWHKPAGRFILMIPALWA-----VCLAAQ--G--LPPLPLGITLAL : 56
 ATP4 : -----TAAATATATG-----EISSRAALAGIGHYAR-----CWELSKAEISMLVATSG-----TYLIGTMAAISFPGLCYTCAG : 138
 SLR1899 : -----TKIHRQHDSMG-----AVCKSYOULTKP-----RIPLIITTAASMI-----ASEGR--VDLPKLLITLIG : 60
 ATP12 : -----DKVKSQTPDKAP--AGGSSINQLLGKAS-----QENKWKIRIOLTKPVWPLVWGVCGAASGNFHWTPEDVAKSILC : 139
 SLR0056 : -----ONT-GONQAKA-----ROLLKGAAP-----GESSIWKILQIMKPIWIPLIWGVCGAASGGYIWSVEDFLKALTC : 73
 ATP8 : -----EVPKLASAEY-----FERGOGKQF-----RSTILIMATALNVRP-----EALIGEST--DIYTELVROR : 63
 SLR1518 : -----SPLAPSTAPAT-----RKILWJALIKP-----PMYVAVVPIVIG-----SAVAYGLTG--QWHDVFTIFLL : 59

ATP12 : ----- * 80 * 200 * 220 * 240 * 260
 SLR1736 : -----AVTAALMNIYIVG-----QISIVEKVNKPYPILASGEYSVNTGIALVASFSLMSFWLGIWGSWPLFWALFSEMIIGTAYS--INPLLR : 228
 ATP3 : -----GAPL--LRGACT-----DIDOD--TKVDRTKLRPIASGLIT--PFOGIGELGOLLIGL-----ILQLNYSRYLGAS--SVPEVR : 134
 SLR0926 : -----GTLA--TSGLCV-----DMDRD--POVERTKORPLAARALS--VOVGIGVALIALLCAG-----LAFYLTPLSFWICVA--AVPIV : 246
 ATP4 : -----TMSI--AASANS-----QFEISNLKMKRTMLRPLPSGRISVPHAVAMATIASGACL-----LASKTNM--AAGLASAN--LVLYAF : 215
 SLR1899 : -----GTA--AASAO-----QFYOD--YEMLRTRARIPAGKQORHALIFALAGLSFAL-----LATFVNV--SGCTALSG--IVFMYL : 137
 ATP12 : -----MMSGCLTGYQT-----DMYTRD--AINEPYRPIPSGAISEEVITQVWVLL--GGIGIAGILD--VMAGHTPTVEFYALG--GSLSY : 223
 SLR0056 : -----MLSGPLMTGYQT-----DEFYRD--AINEPYRPIPSGAISEEVITQVWVLL--GGIGIAGILD--VMAGHTPTVEFYALG--GSLSY : 223
 ATP8 : -----GIAE--ITEMIVASL-----HIDV--ADADTRRGVGLNVVMGKMSVLACDEL--SRACGAL-----AALKNTE--VALIATAVEHLVTGETM : 144
 SLR1518 : -----SALP--IIAWINIS-----DEFISDTCGIDVRKAHSVNLGNRNVLFLISMEFL--AGVGLGMSMS--WRADMTLLEL--GVA-----IFLGY : 138

Figure 22 1/2

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Synechocystis 6803 wild type

Synechocystis slr1736 knockout

Figure 23

Figure 1 consists of four stacked bar charts showing the concentration of different tocopherol forms in mg seed for various plant lines. The x-axis for all charts is 'Plant line number' with values: WT, 1848, 1850, 1851, 1853, 1859, 1860, 1861, 1862, 1864, 1865, 1866, 1868, 1870, 1871, 1874, 1876, 1877, 1854, 1858, 1863, 1872, 1875. The y-axis for alpha-tocopherol ranges from 0 to 40 ng/mg seed. The y-axis for gamma-tocopherol ranges from 0 to 750 ng/mg seed. The y-axis for delta-tocopherol ranges from 0 to 75 ng/mg seed. The y-axis for total tocopherol ranges from 0 to 750 ng/mg seed. Each chart has a shaded bar for the WT line. The bars are black for all other lines.

Plant line number	α -Tocopherol (ng/mg seed)	γ -Tocopherol (ng/mg seed)	δ -Tocopherol (ng/mg seed)	Total tocopherol (ng/mg seed)
WT	14	480	30	520
1848	23	720	85	805
1850	22	660	58	748
1851	18	670	92	780
1853	20	660	50	710
1859	22	730	58	810
1860	33	800	68	868
1861	30	640	42	702
1862	28	780	78	886
1864	32	770	74	876
1865	28	700	48	776
1866	24	580	48	656
1868	22	730	90	840
1870	28	780	62	860
1871	22	730	58	810
1874	22	710	56	796
1876	17	550	45	610
1877	22	740	66	836
1854	30	820	82	902
1858	23	760	74	834
1863	33	860	90	950
1872	21	560	58	638
1875	29	770	78	876

Figure 24

Plant line number	ng total tocopherol/mg seed
Vect. Cont.	~550
WT	~550
1387	~550
1388	~540
1390	~540
1391	~520
1393	~180
1394	~560
1401	~420
1402	~550
1404	~560
1406	~540
1605	~570
1610	~540
1611	~590
1614	~570
1616	~550
1618	~550
1619	~580
1621	~590
1622	~540
1624	~560
1625	~680
1627	~550

Figure 25

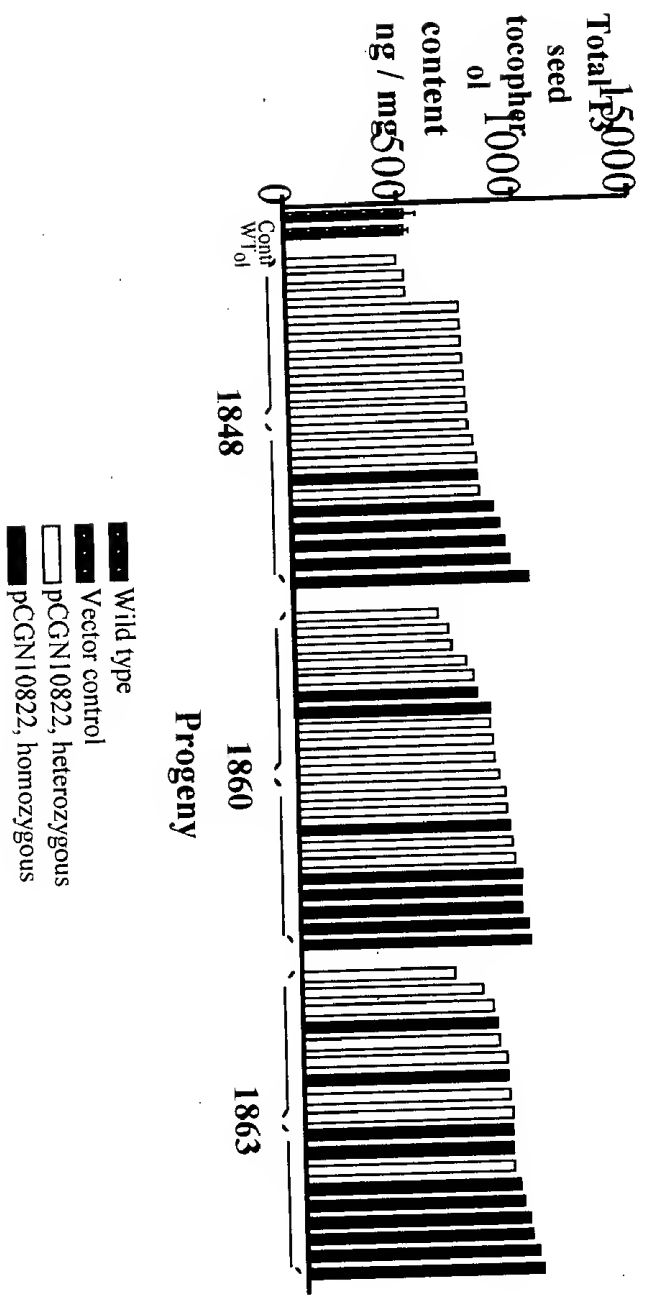


Figure 26

00000000 101400

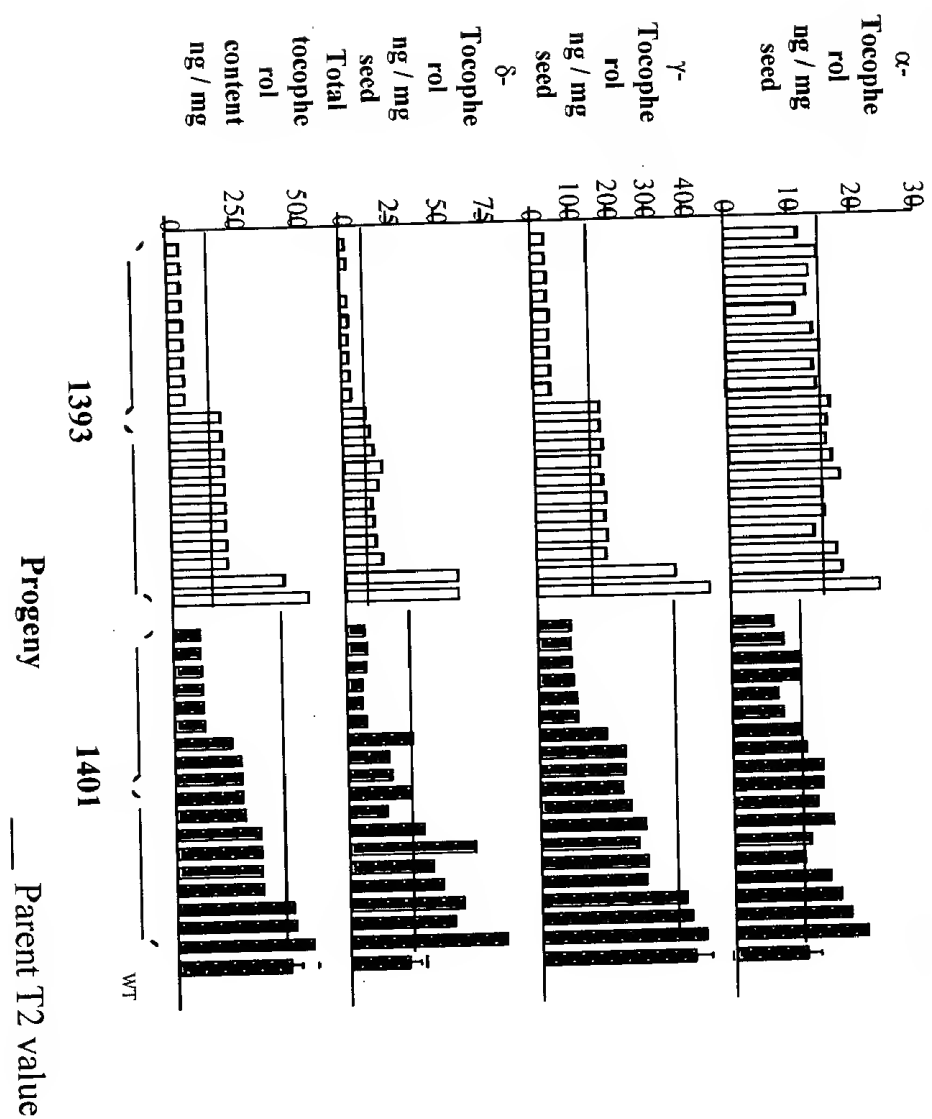


Figure 27

0069099 101400

Total tocopherol in Napin ATPT2 Canola Seed

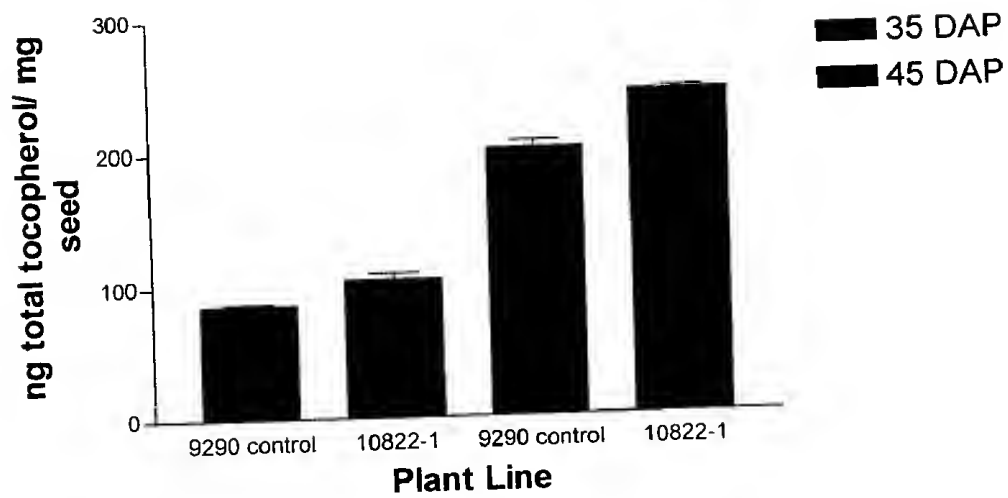


Figure 28

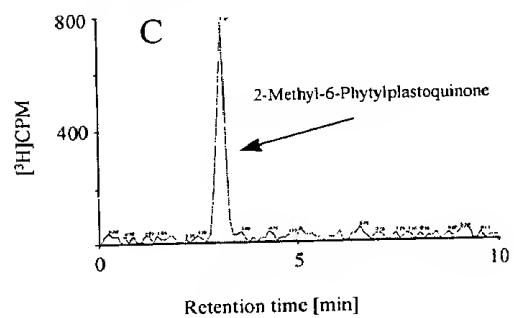
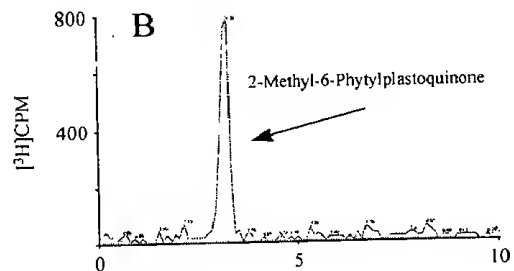
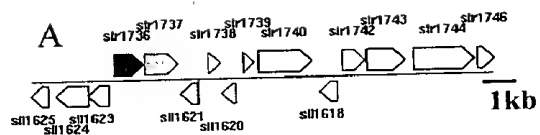


Figure 29

Figure 30

[illegible]

Figure 31
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ATCEA4C371+ 362 AGAGAAGAGGGAGAGATTTTGTGTTTATGTATTCTGTGGAGAATCCTGCATTTTCGGCAGAG
PIR:T04448 46 E K R E S F C F M Y S V E N P A F R Q S

Query- 11415 TTTGTACCATTGGAGTGGCTCTATATGGACCTAGATTCACTGGTGTGGAGCTCAGAT
ATCEA4C371+ 422 TTTGTACCATTGGAGTGGCTCTATATGGACCTAGATTCACTGGTGTGGAGCTCAGAT
PIR:T04448 66 L S P L E V A L Y G P R F T G V G A Q I

Query- 11355 TCTTGGCGCTAATGATAAATATTATGCCAATACGAACAAGACTCTCACAATTTCTGGGG
ATCEA4C371+ 482 TCTTGGCGCTAATGATAAATATTATGCCAATACGAACAAGACTCTCACAATTTCT
PIR:T04448 86 L G A N D K Y L C Q Y E Q D S H N F W G
ATCEA4C371+ Exon 11538 11301 Confidence: 100 100

Query- 11295 AGGTAACCTCTTGACCCCTAAAATGCTGTGTCATGACAATAAGAATCATATCTGAGTCT
ATCEA4C371+ 537
PIR:T04448 106 D
PIR:T04448 Exon 11609 11294 Confidence: 100 100

Query- 11235 TTTCTCTACTTCTAGTACTAATGTTTCGTTATTGTTGTTAAAGATCTAAGTCTTATCTGAA
PIR:T04448 107

Query- 11175 TTTTGTTACATTTTGGTTCGTTCTTCTCAACATGAATTTGTATATATGACTTTAAAG
PIR:T04448 107

Query- 11115 ATTGCTTACCTAAAGTTTTTACTCATGCATAGATCGACATGAGCTAGTTTGGGGAAATAC
PIR:T04448 107 R H E L V L G N T

Query- 11055 TTTTAGTGTGTGTGCCAGGCCCAAAGGCTCCAAACAGGAGGTTCACCAGAGGTCTCTCAC
PIR:T04448 116 F S A V P G A K A P N K E V P P E
PIR:T04448 Exon 11083 11004 Confidence: 96 100

Query- 10995 TCCTCCCTTGTTGGTTACTTTGTTATCTGTTAAATAGTTTCCAATTGTATCCGGATAGT
PIR:T04448 133

Query- 10935 GTTCTACTTCTCCTGTAGAAAATCTCAAGTTTTTGTACTCTTGCTATTCTCTGGATG
PIR:T04448 133

Query- 10875 TTGATTTGTAAGCATGTCGTTTTATTGTAGGAATTTAACAGAAGAGTGTCCGAAGGGTT
PIR:T04448 133 E F N R R V S E G F

Query- 10815 CCAAGCTACTCCATTTTGGCATCAAGGTCACATTGCGATGATGGCCGGTAATTATATGA
PIR:T04448 143 Q A T P F W H Q G H I C D D G R
PIR:T04448 Exon 10844 10768 Confidence: 100 100

Query- 10755 TTCTATGCACAACAAGAATTCACTATATTATAAATATTGGATATTGAGTATTTTGTGTA
PIR:T04448 159

Query- 10695 AAAATTCTGTGTTTAAATCTGACTTGACTTGTTTGTGTCAGTACTGACTATGCGGAAACTG
PIR:T04448 159 T D Y A E T V

Figure 31
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09580050-10448

Query- 10635 TGAATCTGCTCGTTGGGAGTATAGTACTCGTCCCGTTTACGGTTGGGGTGATGTTGGGG
 PIR:T04448 166 K S A R W E Y S T R P V Y G W G D V G A

Query- 10575 CCAAACAGAAGTCAACTGCAGGCTGGCCTGCAGCTTTTCTGTATTTGAGCCTCATTGGC
 PIR:T04448 186 K Q K S T A G W P A A F P V F E P H W Q

Query- 10515 AGATATGCATGGCAGGAGGCTTTCCACAGGTGTGAGCTTTGCTTGATTGACTTAAAGTT
 PIR:T04448 206 I C M A G G L S T G
 PIR:T04448 Exon 10655 10486 Confidence: 96 100

Query- 10455 AATAAATAGACGGTTAAGTTTACTTGCCTAGTACTAACAGAAAATTAAGAAAGAAACCAC
 PIR:T04448 216

Query- 10395 CCTCTTCTATCAGCAGAACTGCTATTGTAGTCTTATTTTTCTCTTGTATTGTCAGG
 PIR:T04448 216

Query- 10335 GTGGATAGAAATGGGGCGGTGAAAGGTTTGAAGTTTCGGGATGCACCTTCTTATTGAGAGAA
 PIR:T04448 216 W I E W G G E R F E F R D A P S Y S E K

Query- 10275 GAATTGGGGTGGAGGCTTCCCAAGAAAATGGTTTGGGTAAAACATTTTCATCCTTTTGCT
 PIR:T04448 236 N W G G G F P R K W F W
 PIR:T04448 Exon 10336 10239 Confidence: 96 100

Query- 10215 ACATTTCTTGTGTCAGACTTTAGTTAGCTAGTGGACCTGTGTATACACCACATGTAGTA
 PIR:T04448 248

Query- 10155 TACTTGTTTGATAGCTTTATTGTCAATGTCTCTTACAGGTCCAGTGAATGCTTTGA
 PIR:T04448 248 V Q C N V F E

Query- 10095 AGGGGCAACTGGAGAAGTTGCTTTAACCAGGAGGCGGGTTGAGGCAATGCCTGGATT
 PIR:T04448 255 G A T G E V A L T A G G G L R Q L P G L

Query- 10035 GACTGAGACCTATGAAATGCTGCACTGGTATGCACCTATAAGATCTTCTTAAGCAATGA
 PIR:T04448 275 T E T Y E N A A L
 PIR:T04448 Exon 10115 10008 Confidence: 100 100

Query- 9975 CAGTGAGTATTAGAAGGCAGATAGTTTACAAGCTCTGGGCCCTTGTAATCTGCAGGT
 PIR:T04448 284 V

Query- 9915 TTGTGTACACTATGATGGAAAAATGTACGAGTTTGTTCCTTGGAAATGTTGTTGTAGATG
 PIR:T04448 285 C V H Y D G K M Y E F V P W N G V V R W
 GSDB:S:495- 532 tagatg

Query- 9855 GGAAATGTCTCCCTGGGG TTATTGGTATATACTGCAGAGAACGAAACCATGTGGTAA
 PIR:T04448 305 E M S P W G Y W Y I T A E N E N H V
 GSDB:S:495- 526 ggaaat tctccctgggggttattggtatataactgcagagaaNcgNaaacatgtg
 PIR:T04448 Exon 9917 9801 Confidence: 100 100
 GSDB:S:495- Exon 9861 9801 Confidence: 93 93

Query- 9796 ATTTGTTTACTAGTTTCATTTCAGTTTACTTTTGACATCATATCATTCCTTATGGCTA

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PIR:T04448      323 -----
GSDB:S:495-    471 -----
Query-          9736 GATTCCAACACCCGATGAATGTCTTGTGACAGGTGGAAC TAGAGGCCAAGAACAATGAAG
                  .....
                  V E L E A R T N E A
PIR:T04448      323 -----
GSDB:S:495-    471 -----
                  gtggaactagaggcNagaacaatatgaag

Query-          9676 CGGGTACACCTCTGCCGTGCTCCTACCACAGAAGTTGGGCTAGCTACGGCTTGCGAGATA
                  .....
                  G T P L R A P T T E V G L A T A C R D S
PIR:T04448      333 -----
GSDB:S:495-    443 cggggtacacctctgcgtgctcctaccacagaagtgggctagctacggcttgcgagata

Query-          9616 GTTGTTCACGGTGAATTGAAGTTGCAGATATGGGAACGGCTATATGATGGAAGTAAGGCA
                  .....
                  C Y G E L K L Q I W E R L Y D G S K G K
PIR:T04448      353 -----
GSDB:S:495-    383 gttgttacggtgaattgaagttgcagatattgggaacggctatatgatggaagtaaaggca

Query-          9556 AGGTATGTATGCTAATGTGATCCAATCCCTGTAGTTAAAGTCTTAACAATCCTAAGGC
                  .....
                  L K V L T N P K A
PIR:T04448      373 -----
GSDB:S:495-    323 ag
                  Exon       9704       9555 Confidence: 100 100
GSDB:S:495-    323 Exon       9704       9555 Confidence: 98 100

Query-          9496 AGTGAAAGAAGATTATGAACGTTTGTATGTTAACAATGATGCAGGTGATATTAGAGAC
                  .....
                  V K E D Y E R L L W L T M M Q V I L E T
PIR:T04448      382 -----
GSDB:S:495-    321 -----
                  gtgatatttagagac

Query-          9436 AAAGAGCTCAATGGCAGCAGTGGAGATAGGAGGAGGACCGTGGTTTGGGACATGGAAGG
                  .....
                  K S S M A A V E I G G G P W F G T W K G
PIR:T04448      402 -----
GSDB:S:495-    307 aaagagctcaatggcancagtggagataggaggaggaccggtggttgggacatggaaggg

Query-          9376 AGATACGAGCAACACGCCGAGCTACTAAAACAGGCTCTTCAGGTCCCATTGGATCTTGA
                  .....
                  D T S N T P E L L K Q A L Q V P L D L E
PIR:T04448      422 -----
GSDB:S:495-    247 agatacgagcaaacacgcccgagctactaaaacaggctcttcagggtcccattggatcttga

Query-          9316 AAGCGCCTTAGGTTTGTTGCCCTTCTTCAAGCCACCGGGTCTG TAACATTGATGAGTGTG
                  .....
                  S A L G L V P F F K P P G L
PIR:T04448      442 -----
GSDB:S:495-    187 aagcgccttaggtttggcccttcttcaagccacgggctctgtaacattgatgagtggt
                  Exon       9522       9274 Confidence: 100 100
PIR:T04448      -----

Query-          9256 TTGTTTGTGTGATAGACCCCATGTGATGAATGAAGCCTTAGTCATGTCTTGTCTAGCTTG
                  .....
                  t t g t t g t t g a t a g a c c c a t g t g a t g a a t g a a g c c t t a g t c a t g t c a t t g t c t a g c t t
PIR:T04448      456 -----
GSDB:S:495-    127 -----

Query-          9196 ACTATTATGTATGTATGATTTTAGTTCGTTTCGGTTCCTTGTGGTAAATGATACGGGCCAGT
                  .....
                  a c t a t t a t g t a t g t a t g a t t t a g t t c g t t c g g t c c t t g t g g t a a a t g a t a c g g g c c a g t
PIR:T04448      67 -----
GSDB:S:495-    -----

Query-          9136 GTAAAGTCTAGTTCAATAAAAGCCTTGAGTCGCATAAATTCATTTCAAATTCATC
                  .....
                  7 gtaaaagt
GSDB:S:495-    Exon       9450       9130 Confidence: 98 100
GSDB:S:495-    -----

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Figure 31
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PIR:T04448 sPIR:T04448 hypothetical protein F4D11.30 - Arabidopsis thaliana;
 -b1c2a18584.1 (AL022537) putative protein [Arabidopsis thaliana]_F4

PIR:T04448 SPIR-T04448 shypothetical protein F4D11.30 - Arabidopsis thaliana;
g3063693|emb|CAA18584.1 (AL022537) putative protein [Arabidopsis thaliana]_F4D11.30

g3063693|emb|CAA18584.1 (A1022537) putative protein [Arabidopsis thaliana]
 GSDB:S:4955486|AI995392|AI995392|701673779 A. thaliana, Columbia Col-0, inflorescence-1
 Arabidopsis thaliana cDNA clone 701673779, mRNA sequence.

Figure 32

Figure 33

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

---DWGLTEENLSKKT---VPF---
TWKGDTSNTPELLKQALQVPLDLESALGLVPFFKPPGL
---EEKLAKEN---

Figure 35